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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/993,966

DATE: 09/05/2002

TIME: 10:15:18

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Output Set: N:\CRF3\09052002\I993966.raw

3 <110> APPLICANT: ROHAN, MICHAEL  
5 <120> TITLE OF INVENTION: HUMAN AND NON-HUMAN PRIMATE HOMOLOGUES OF NKD PROTEIN,  
6 NUCLEIC ACID SEQUENCES ENCODING, AND USES THEREOF  
8 <130> FILE REFERENCE: 014024/0280733  
10 <140> CURRENT APPLICATION NUMBER: 09/993,966  
11 <141> CURRENT FILING DATE: 2001-11-27  
13 <150> PRIOR APPLICATION NUMBER: 60/252,884  
14 <151> PRIOR FILING DATE: 2000-11-27  
16 <150> PRIOR APPLICATION NUMBER: 60/291,109  
17 <151> PRIOR FILING DATE: 2001-05-16  
19 <150> PRIOR APPLICATION NUMBER: 60/325,571  
20 <151> PRIOR FILING DATE: 2001-10-01  
22 <160> NUMBER OF SEQ ID NOS: 26  
24 <170> SOFTWARE: PatentIn Ver. 2.1  
26 <210> SEQ ID NO: 1  
27 <211> LENGTH: 1786  
28 <212> TYPE: DNA  
29 <213> ORGANISM: Homo sapiens  
31 <400> SEQUENCE: 1  
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34 catggcttag ggacgtccc ggccgcccga gccccagcat ggggaaactt cactccaagc 180  
35 cggccgcccgt gtgcaagcgc agggagagcc cggaagggtga cagcttcgcc gtgagcgtcg 240  
36 cctgggctcg gaagggcatc gaggagtga tcgggagaca gcgtgcccg ggcgggtgtct 300  
37 cgggaccccg acagctgcgg ttggcgggca ccataggccg aagcaccggg gagctcgttg 360  
38 gcgacgtgtt gagagacacg ctacgcgagg aagaggagga cgactttcgg ctggaagtgg 420  
39 ccctgcctcc tgagaagact gacgggctgg gcagcggaga tgagaagaag atggagagag 480  
40 tgagcgaacc ctgcccaggc tccaagaagc agctgaagtt tgaagagctc cagtgcgacg 540  
41 tgtccatgga ggaggacagc cggcaggagt ggaccttcac cctgtatgac ttgacaaca 600  
42 acggcaaggt cacccgagag gacatcacca gcttgcgtga caccatctat gaggtggtgg 660  
43 actcctctgt caaccactcc ccaacatcca gcaagatgct gcgggtaag ctcaccgtgg 720  
44 ccccgatgg cagccagagc aagaggagcg tccttgtcaa tcaggctgac ctgcagagcg 780  
45 caaggcccg agcagagacc aagcccactg aggacctgag gagctgggag aagaagcagc 840  
46 gagccccgct caggttcag ggtgacagcc gcctggagca gtctggctgc taccaccatt 900  
47 gcgtagatga gaacatcgag aggagaaacc actacttaga tctcgccggg atagaaaact 960  
48 acacgtccca atttgggect ggctcccctt ccgtggccca gaagtcagaa ctgccccccc 1020  
49 gcacctcaa tcccactcga tctcgtctcc atgagccgga agccatccac atcccacacc 1080  
50 gaaagcccca aggcgtggac ccggcctcct tccacttctt tgacacccca atcgccaagg 1140  
51 tctcagagct ccagcaacgg ctccggggca ccaggagcgg gagcaagcac tttgtgaggt 1200  
52 cccccaaggc ccagggcaag agtggtgggtg tgggccaagt ggccagagg gcaagaaaca 1260  
53 agccccctct gggacccgac atccctgcgg tgtcccccct cggccacctg gctgccagcc 1320  
54 cggccctcct cccctcccta gccccctcg ggcacaagaa gcacaagcac cgagccaagg 1380  
55 agagccagca gggctgcgg ggcctgcagg caccactggc ctgaggtgg cctgtcctgg 1440

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56 ggcggggagca cctgcggggag ctgcccgcct tgggtggtgta tgagagccag gccggggcagc 1500
57 cggtccagag acatgagcac caccaccacc atgaacatca ccaccattac caccacttct 1560
58 accagacata gagccccctcc ccaggggcccc accctgccat atgaaggacc ccacccccga 1620
59 caccacaagg cattattatt ctattaatta ttgttattat gatgattatt gttattaata 1680
60 attattgtta ctccactaat atttagctag cctacatgta gaagatctat ggaaacacag 1740
61 aactaaactt ttatttatat gttaaaaaaa aaaaaaaaaa aaaaaa 1786

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64 &lt;210&gt; SEQ ID NO: 2

65 &lt;211&gt; LENGTH: 1416

66 &lt;212&gt; TYPE: DNA

67 &lt;213&gt; ORGANISM: Mus sp.

69 &lt;400&gt; SEQUENCE: 2

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70 atggggaaac ttcaactgaa gccggccgcc gtgtgcaagc gcaggagag cccggaaggt 60
71 gacagctttg ctgtaagcgc tgcttgggca aggaaggca tcgaggagt gatcgggag 120
72 cagcgtctgtc caggcagcgt ctccaggacc cgtcagctga gattggcagg cactgttgg 180
73 cgaggcactc gggaactcgt gggtagact tctagagagg ctctcgggta ggaggacgag 240
74 gacgacttcc ccctagaagt ggccctgccg cctgagaaga tcgacagcct aggtagtgg 300
75 gatgagaaga gaatggagag actgagcgaa cctggccagg cctccaagaa gcagctcaag 360
76 tttgaagagc tacagtgtga tgtctctgtg gaggaggaca gccggcaaga gtggactttc 420
77 actctatatg acttcgacaa caatggcaaa gtgaccctgt aggacattac cagcttgcgt 480
78 cataccatct atgaagtggg tgaactcctc gtgaaccatt cccccacatc aagcaagaca 540
79 ctgcgggtga agctcaccgt ggctcctgac gggagccaga gtaagaggag cgtccttttc 600
80 aaccataccg atctgcagag cacaaggccc cgagcagaca ccaaaccgc tgaggagctg 660
81 cgtggctggg agaagaagca gcgagcccca ctgaggttcc aggtgacag ccacctggag 720
82 cagccagact gctaccacca ttgcgtggat gagaacattg agaggagaaa ccactaccta 780
83 gacctggcgg ggatagagaa ctacacgtct cagtttggac cgggatcccc ttcggtggcc 840
84 cagaagtcag agctgcccc tgaatctcc aacccactc gctctcgtc ccacgagcca 900
85 gaagctgccc acatcccaca ccggaggccc caaggtgtgg acccaggctc cttccacctc 960
86 cttgacaccc catittgcaa ggcacagag ctccagcaac ggctccgggg cactcaggat 1020
87 gggagcaagc actttgtgag gtcccccaag gccagggca agaacatgg tatgggccac 1080
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89 tctgcccatac tggccaccag ccagccctt ctccccacce tggcaccctt ggggcacaag 1200
90 aaacacaagc atcgagccaa ggagagccag gcgagctgcc ggggacctga gggccccctg 1260
91 gctgcaggag gctccaccgt catggggcgg gagcagggtg gggagctgcc tgccgtggtg 1320
92 gtgtacgaga gccaggctgg gcaggccgtc cagagacacg aacaccatca ccaccacca 1380
93 catcaccacc attatcacca cttctatcag ccctag 1416

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96 &lt;210&gt; SEQ ID NO: 3

97 &lt;211&gt; LENGTH: 470

98 &lt;212&gt; TYPE: PRT

99 &lt;213&gt; ORGANISM: Homo sapiens

101 &lt;400&gt; SEQUENCE: 3

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103   1           5           10           15
105 Ser Pro Glu Gly Asp Ser Phe Ala Val Ser Ala Ala Trp Ala Arg Lys
106           20           25           30
108 Gly Ile Glu Glu Trp Ile Gly Arg Gln Arg Cys Pro Gly Gly Val Ser
109           35           40           45
111 Gly Pro Arg Gln Leu Arg Leu Ala Gly Thr Ile Gly Arg Ser Thr Arg
112           50           55           60
114 Glu Leu Val Gly Asp Val Leu Arg Asp Thr Leu Ser Glu Glu Glu Glu

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115	65					70				75				80		
117	Asp	Asp	Phe	Arg	Leu	Glu	Val	Ala	Leu	Pro	Pro	Glu	Lys	Thr	Asp	Gly
118					85					90					95	
120	Leu	Gly	Ser	Gly	Asp	Glu	Lys	Lys	Met	Glu	Arg	Val	Ser	Glu	Pro	Cys
121				100					105					110		
123	Pro	Gly	Ser	Lys	Lys	Gln	Leu	Lys	Phe	Glu	Glu	Leu	Gln	Cys	Asp	Val
124			115					120					125			
126	Ser	Met	Glu	Glu	Asp	Ser	Arg	Gln	Glu	Trp	Thr	Phe	Thr	Leu	Tyr	Asp
127		130					135					140				
129	Phe	Asp	Asn	Asn	Gly	Lys	Val	Thr	Arg	Glu	Asp	Ile	Thr	Ser	Leu	Leu
130	145				150					155					160	
132	His	Thr	Ile	Tyr	Glu	Val	Val	Asp	Ser	Ser	Val	Asn	His	Ser	Pro	Thr
133				165					170						175	
135	Ser	Ser	Lys	Met	Leu	Arg	Val	Lys	Leu	Thr	Val	Ala	Pro	Asp	Gly	Ser
136			180						185					190		
138	Gln	Ser	Lys	Arg	Ser	Val	Leu	Val	Asn	Gln	Ala	Asp	Leu	Gln	Ser	Ala
139		195						200					205			
141	Arg	Pro	Arg	Ala	Glu	Thr	Lys	Pro	Thr	Glu	Asp	Leu	Arg	Ser	Trp	Glu
142		210					215					220				
144	Lys	Lys	Gln	Arg	Ala	Pro	Leu	Arg	Phe	Gln	Gly	Asp	Ser	Arg	Leu	Glu
145	225				230					235					240	
147	Gln	Ser	Gly	Cys	Tyr	His	His	Cys	Val	Asp	Glu	Asn	Ile	Glu	Arg	Arg
148			245						250					255		
150	Asn	His	Tyr	Leu	Asp	Leu	Ala	Gly	Ile	Glu	Asn	Tyr	Thr	Ser	Gln	Phe
151			260					265						270		
153	Gly	Pro	Gly	Ser	Pro	Ser	Val	Ala	Gln	Lys	Ser	Glu	Leu	Pro	Pro	Arg
154		275						280					285			
156	Thr	Ser	Asn	Pro	Thr	Arg	Ser	Arg	Ser	His	Glu	Pro	Glu	Ala	Ile	His
157		290					295					300				
159	Ile	Pro	His	Arg	Lys	Pro	Gln	Gly	Val	Asp	Pro	Ala	Ser	Phe	His	Phe
160	305				310					315					320	
162	Leu	Asp	Thr	Pro	Ile	Ala	Lys	Val	Ser	Glu	Leu	Gln	Gln	Arg	Leu	Arg
163			325						330					335		
165	Gly	Thr	Gln	Asp	Gly	Ser	Lys	His	Phe	Val	Arg	Ser	Pro	Lys	Ala	Gln
166			340					345					350			
168	Gly	Lys	Ser	Val	Gly	Val	Gly	His	Val	Ala	Arg	Gly	Ala	Arg	Asn	Lys
169		355					360						365			
171	Pro	Pro	Leu	Gly	Pro	Ala	Ile	Pro	Ala	Val	Ser	Pro	Ser	Ala	His	Leu
172		370				375						380				
174	Ala	Ala	Ser	Pro	Ala	Leu	Leu	Pro	Ser	Leu	Ala	Pro	Leu	Gly	His	Lys
175	385				390					395					400	
177	Lys	His	Lys	His	Arg	Ala	Lys	Glu	Ser	Gln	Gln	Gly	Cys	Arg	Gly	Leu
178			405					410						415		
180	Gln	Ala	Pro	Leu	Ala	Ser	Gly	Gly	Pro	Val	Leu	Gly	Arg	Glu	His	Leu
181			420					425					430			
183	Arg	Glu	Leu	Pro	Ala	Leu	Val	Val	Tyr	Glu	Ser	Gln	Ala	Gly	Gln	Pro
184		435					440						445			
186	Val	Gln	Arg	His	Glu	His	His	His	His	Glu	His	His	His	His	His	Tyr
187		450				455						460				

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189 His His Phe Tyr Gln Thr
190 465                               470
193 <210> SEQ ID NO: 4
194 <211> LENGTH: 471
195 <212> TYPE: PRT
196 <213> ORGANISM: Mus sp.
198 <400> SEQUENCE: 4
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200 1                               5 10 15
202 Ser Pro Glu Gly Asp Ser Phe Ala Val Ser Ala Ala Trp Ala Arg Lys
203 20 25 30
205 Gly Ile Glu Glu Trp Ile Gly Arg Gln Arg Cys Pro Gly Ser Val Ser
206 35 40 45
208 Gly Pro Arg Gln Leu Arg Leu Ala Gly Thr Val Gly Arg Gly Thr Arg
209 50 55 60
211 Glu Leu Val Gly Asp Thr Ser Arg Glu Ala Leu Gly Glu Glu Asp Glu
212 65 70 75 80
214 Asp Asp Phe Pro Leu Glu Val Ala Leu Pro Pro Glu Lys Ile Asp Ser
215 85 90 95
217 Leu Gly Ser Gly Asp Glu Lys Arg Met Glu Arg Leu Ser Glu Pro Gly
218 100 105 110
220 Gln Ala Ser Lys Lys Gln Leu Lys Phe Glu Glu Leu Gln Cys Asp Val
221 115 120 125
223 Ser Val Glu Glu Asp Ser Arg Gln Glu Trp Thr Phe Thr Leu Tyr Asp
224 130 135 140
226 Phe Asp Asn Asn Gly Lys Val Thr Arg Glu Asp Ile Thr Ser Leu Leu
227 145 150 155 160
229 His Thr Ile Tyr Glu Val Val Asp Ser Ser Val Asn His Ser Pro Thr
230 165 170 175
232 Ser Ser Lys Thr Leu Arg Val Lys Leu Thr Val Ala Pro Gly Asp Ser
233 180 185 190
235 Gln Ser Lys Arg Ser Val Leu Phe Asn His Thr Asp Leu Gln Ser Thr
236 195 200 205
238 Arg Pro Arg Ala Asp Thr Lys Pro Ala Glu Glu Leu Arg Gly Trp Glu
239 210 215 220
241 Lys Lys Gln Arg Ala Pro Leu Arg Phe Gln Gly Asp Ser His Leu Glu
242 225 230 235 240
244 Gln Pro Asp Cys Tyr His His Cys Val Asp Glu Asn Ile Glu Arg Arg
245 245 250 255
247 Asn His Tyr Leu Asp Leu Ala Gly Ile Glu Asn Tyr Thr Ser Gln Phe
248 260 265 270
250 Gly Pro Gly Ser Pro Ser Val Ala Gln Lys Ser Glu Leu Pro Pro Arg
251 275 280 285
253 Ile Ser Asn Pro Thr Arg Ser Arg Ser His Glu Pro Glu Ala Ala His
254 290 295 300
256 Ile Pro His Arg Arg Pro Gln Gly Val Asp Pro Gly Ser Phe His Leu
257 305 310 315 320
259 Leu Asp Thr Pro Phe Ala Lys Ala Ser Glu Leu Gln Gln Arg Leu Arg
260 325 330 335

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262 Gly Thr Gln Asp Gly Ser Lys His Phe Val Arg Ser Pro Lys Ala Gln  
 263 340 345 350  
 265 Gly Lys Asn Met Gly Met Gly His Gly Ala Arg Gly Ala Arg Ser Lys  
 266 355 360 365  
 268 Pro Pro Leu Val Pro Thr Thr His Thr Val Ser Pro Ser Ala His Leu  
 269 370 375 380  
 271 Ala Thr Ser Pro Ala Leu Leu Pro Thr Leu Ala Pro Leu Gly His Lys  
 272 385 390 395 400  
 274 Lys His Lys His Arg Ala Lys Glu Ser Gln Ala Ser Cys Arg Gly Leu  
 275 405 410 415  
 277 Gln Gly Pro Leu Ala Ala Gly Gly Ser Thr Val Met Gly Arg Glu Gln  
 278 420 425 430  
 280 Val Arg Glu Leu Pro Ala Val Val Val Tyr Glu Ser Gln Ala Gly Gln  
 281 435 440 445  
 283 Ala Val Gln Arg His Glu His His His His His Glu His His His His  
 284 450 455 460  
 286 Tyr His His Phe Tyr Gln Pro  
 287 465 470

290 &lt;210&gt; SEQ ID NO: 5

291 &lt;211&gt; LENGTH: 1859

292 &lt;212&gt; TYPE: DNA

293 &lt;213&gt; ORGANISM: Homo sapiens

295 &lt;400&gt; SEQUENCE: 5

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 297 cggggagtcg ggccgcggcg acggcggcag gagcgctcc cggcgccgcc tcgggctccg 120  
 298 ctcggtctcg gggctgcttc gggaggagga gagccaagg aggcgccagg cccgcgggcc 180  
 299 gggcgcatgg cttaggggacg ctcccggccg ccgcagcccc agcatgggga aacttcactc 240  
 300 caagccggcc gccgtgtgca agcgcaggga gagcccggaa ggtgacagct tcgccgtgag 300  
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 303 cgtgggcgac gtgttgagag acacgctcag cgaggaagag gaggacgact ttcggctgga 480  
 304 agtggccctg cctcctgaga agactgacgg gctgggcagc ggagatgaga agaagatgga 540  
 305 gagagtgagc gaaccctgcc caggctccaa gaagcagctg aagtttgaag agctccagtg 600  
 306 cgacgtgtcc atggaggagg acagccggca ggagtggacc ttcacctgt atgactttga 660  
 307 caacaacggc aaggtcaccc gagaggacat caccagcttg ctgcacacca tctatgaggt 720  
 308 ggtggactcc tctgtcaacc actccccaac atccagcaag atgctgcggg taaagctcac 780  
 309 cgtggccccc gatggcagcc agagcaagag gagcgtcctt gtcaatcagg ctgacctgca 840  
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 311 gcagcgagcc ccgctcaggt tccagggtga cagccgcctg gagcagctc gctgctacca 960  
 312 ccattgcgta gatgagaaca tcgagaggag aaaccactac ttagatctcg ccgggataga 1020  
 313 aaactacacg tcccaatttg ggcctggctc cccttccgtg gcccagaagt cagaactgcc 1080  
 314 ccccgccacc tccaatccca ctcgatctcg ctcccatgag ccggaagcca tccacatccc 1140  
 315 acaccgaaag ccccaaggcg tggaccggcg ctccctccac ttccttgaca ccccaatcgc 1200  
 316 caaggtctca gagctccagc aacggctccg gggcaccag gacgggagca agcactttgt 1260  
 317 gaggtccccc aaggcccgag gcaagagtgt ggggtgtggc cacgtggcca gaggggcaag 1320  
 318 aaacaagccc cctctgggac ccgccatccc tgcggtgtcc cctccgccc acctggctgc 1380  
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VERIFICATION SUMMARY

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